

Application of: Hoogenboom and Henderikx

Serial No.: **Continuation of U.S. Application  
09/538,913**

Filed: (concurrently herewith)

Entitled: MUCIN-1 SPECIFIC BINDING  
MEMBERS AND METHODS OF  
USE THEREOF

Attorney Docket No.: DYX-015.1 US

ART UNIT:

EXAMINER:

STATEMENT UNDER 37 C.F.R. § 1.821(f)

Assistant Commissioner for Patents  
Washington, D.C. 20231

Sir:

Applicants submit herewith a Sequence Listing in written and computer readable form under 37 C.F.R. § 1.821(a)-(e) complying with the provisions of 37 C.F.R. § 1.824. The sequence listing is being submitted along with the original application papers.

In accordance with 37 C.F.R. § 1.821(f), the undersigned attorney of record hereby states that the written form and the computer readable form of the Sequence Listing submitted herewith for the above-identified patent application are identical in content.

30-March-2001

Date



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## SEQUENCE LISTING

<110> DYAX CORP.

<120> MUCIN-1 Specific Binding Members and Methods of Use Thereof

<130> DYX-015.1 US, DYX-015.1 PCT

<140> not yet assigned

<141> 2001-03-30

<150> US 09/538,913

<151> 2000-03-30

<160> 112

<170> PatentIn version 3.0

<210> 1

<211> 113

<212> PRT

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Glu Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Leu His Ser  
20 25 30

Asn Gly Tyr Thr Tyr Leu Asp Trp Tyr Leu Gln Lys Pro Gly Gln Ser  
35 40 45

Pro Gln Leu Leu Ile Tyr Ser Gly Ser His Arg Ala Ser Gly Val Pro  
50 55 60

Asp Arg Phe Ser Gly Ser Val Ser Gly Thr Asp Phe Thr Leu Arg Ile  
65 70 75 80

Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Met Gln Gly  
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 tacctgcaga agccagggca gtctccacag ctctgatct attcgggttc tcatcggggc 180  
 tccgggggtcc ctgacagggt cagtggcagt gtatcaggca cagattttac actgagaatc 240  
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 Ala Met Gly Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val  
 35 40 45  
 Ser Gly Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val  
 50 55 60  
 Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr  
 65 70 75 80  
 Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys  
 85 90 95  
 Ala Lys His Thr Gly Gly Gly Val Trp Asp Pro Ile Asp Tyr Trp Gly

100 105 110

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gcagactccg tgaagggccg gttcaccatc tccagagaca attccaagaa cacgctgtat 240  
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20 25 30  
Ala Met Gly Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val  
35 40 45  
Ser Gly Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val  
50 55 60  
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr  
65 70 75 80

Leu	Gln	Met	Asn	Ser	Leu	Arg	Ala	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys	85	90	95	
Ala	Lys	His	Thr	Gly	Gly	Gly	Val	Trp	Asp	Pro	Ile	Asp	Tyr	Trp	Gly	100	105	110	
Gln	Gly	Thr	Leu	Val	Thr	Val	Ser	Ser	Gly	Gly	Gly	Ala	Leu	Glu	Ile	115	120	125	
Val	Leu	Thr	Gln	Ser	Pro	Leu	Ser	Leu	Pro	Val	Thr	Pro	Gly	Glu	Pro	130	135	140	
Ala	Ser	Ile	Ser	Cys	Arg	Ser	Ser	Gln	Ser	Leu	Leu	His	Ser	Asn	Gly	145	150	155	160
Tyr	Thr	Tyr	Leu	Asp	Trp	Tyr	Leu	Gln	Lys	Pro	Gly	Gln	Ser	Pro	Gln	165	170	175	
Leu	Leu	Ile	Tyr	Ser	Gly	Ser	His	Arg	Ala	Ser	Gly	Val	Pro	Asp	Arg	180	185	190	
Phe	Ser	Gly	Ser	Val	Ser	Gly	Thr	Asp	Phe	Thr	Leu	Arg	Ile	Ser	Arg	195	200	205	
Val	Glu	Ala	Glu	Asp	Val	Gly	Val	Tyr	Tyr	Cys	Met	Gln	Gly	Leu	Gln	210	215	220	
Ser	Pro	Phe	Thr	Phe	Gly	Pro	Gly	Thr	Lys	Val	Asp	Ile	Lys	Arg	Gly	225	230	235	240
Gly	Gly	Ser	Gly	Gly	Gly	Ala	Leu	Ala	Pro	Thr	Ser	Ser	Ser	Thr	Lys	245	250	255	
Lys	Thr	Gln	Leu	Gln	Leu	Glu	His	Leu	Leu	Leu	Asp	Leu	Gln	Met	Ile	260	265	270	
Leu	Asn	Gly	Ile	Asn	Asn	Tyr	Lys	Asn	Pro	Lys	Leu	Thr	Arg	Met	Leu	275	280	285	
Thr	Phe	Lys	Phe	Tyr	Met	Pro	Lys	Lys	Ala	Thr	Glu	Leu	Lys	His	Leu	290	295	300	
Gln	Cys	Leu	Glu	Glu	Glu	Leu	Lys	Pro	Leu	Glu	Glu	Val	Leu	Asn	Leu	305	310	315	320
Ala	Gln	Ser	Lys	Asn	Phe	His	Leu	Arg	Pro	Arg	Asp	Leu	Ile	Ser	Asn				

325	330	335
Ile Asn Val Ile Val Leu Glu Leu Lys Gly Ser Glu Thr Thr Phe Met		
340	345	350
Cys Glu Tyr Ala Asp Glu Thr Ala Thr Ile Val Glu Phe Leu Asn Arg		
355	360	365
Trp Ile Thr Phe Cys Gln Ser Ile Ile Ser Thr Leu Thr		
370	375	380

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 gcagactccg tgaagggccg gttcaccatc tccagagaca attccaagaa cacgctgtat 240  
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gttctggaac taaagggatc tgaaacaaca ttcattgtgtg aatatgctga tgagacagca      1080
accattgtag aattttctgaa cagatggatt accttttgtc aaagcatcat ctcaacactg      1140
act                                                                    1143

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Pro Ala His Gly Val Thr Ser Ala Pro Asp Thr Arg Pro Ala Pro Gly
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Ser Thr Ala Pro
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<210> 8
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<400> 8

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Val Thr Ser Ala Pro Asp Thr Arg Pro Ala Pro Gly Ser Thr Ala Pro
1           5           10           15

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Pro Ala His Gly
          20

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24

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<210> 12  
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<400> 12  
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<210> 13  
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<210> 15



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agttctaca

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Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr  
 20 25 30

Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val  
 35 40 45

Ser Ala Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val  
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr  
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys  
 85 90 95

Ala Lys

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<400> 19

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Glu Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Leu His Ser  
 20 25 30

Asn Gly Tyr Asn Tyr Leu Asp Trp Tyr Leu Gln Lys Pro Gly Gln Ser  
 35 40 45

Pro Gln Leu Leu Ile Tyr Leu Gly Ser Asn Arg Ala Ser Gly Val Pro  
 50 55 60

Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile  
 65 70 75 80

Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Met Gln Ala  
 85 90 95

Leu Gln Thr Pro  
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Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu Asn Gly Ala Ala  
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42

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<400> 22

His His His His His His  
 1 5

<210> 23  
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 <212> DNA  
 <213> synthetic

<400> 23  
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<400> 24

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Glu Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Leu His Ser  
 20 25 30

Asn Gly Tyr Thr Tyr Leu Asp Trp Tyr Leu Gln Lys Pro Gly Gln Ser  
 35 40 45

Pro Gln Leu Leu Ile Tyr Ser Gly Ser His Arg Ala Ser Gly Val Pro  
 50 55 60

Asp Arg Phe Ser Gly Ser Val Ser Gly Thr Asp Phe Thr Leu Arg Ile  
65 70 75 80

Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Met Gln Gly  
85 90 95

Leu Gln Ser Pro Phe Thr Phe Gly Pro Gly Thr Lys Val Asp Ile Lys  
100 105 110

Arg Gly Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp  
115 120 125

Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn  
130 135 140

Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu  
145 150 155 160

Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp  
165 170 175

Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr  
180 185 190

Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser  
195 200 205

Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys  
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tccgggggtcc ctgacagggt cagtggcagt gtatcaggca cagattttac actgagaatc 240  
agcagagtgg aggctgagga tggttgagtt tattactgca tgcaggggtct acagagtcca 300  
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caatcgggta actcccagga gagtgtcaca gagcaggaca gcaaggacag cacctacagc      540
ctcagcagca ccttgacgct gagcaaagca gactacgaga aacacaaagt ctacgcctgc      600
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<400> 26

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                20              25              30
Ala Met Gly Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
                35              40              45
Ser Gly Ile Ser Gly Ser Gly Gly Ser Thr Tyr Tyr Ala Asp Ser Val
50              55              60
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65              70              75              80
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85              90              95
Ala Lys His Thr Gly Gly Gly Val Trp Asp Pro Ile Asp Tyr Trp Gly
                100             105             110
Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser
115              120              125
Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala
130              135              140

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Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val  
 145 150 155 160  
 Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala  
 165 170 175  
 Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val  
 180 185 190  
 Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His  
 195 200 205  
 Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys  
 210 215 220  
 Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly  
 225 230 235 240  
 Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met  
 245 250 255  
 Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His  
 260 265 270  
 Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val  
 275 280 285  
 His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr  
 290 295 300  
 Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly  
 305 310 315 320  
 Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile  
 325 330 335  
 Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val  
 340 345 350  
 Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser  
 355 360 365  
 Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu  
 370 375 380  
 Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro

385		390		395		400									
Val	Leu	Asp	Ser	Asp	Gly	Ser	Phe	Phe	Leu	Tyr	Ser	Lys	Leu	Thr	Val
				405					410					415	
Asp	Lys	Ser	Arg	Trp	Gln	Gln	Gly	Asn	Val	Phe	Ser	Cys	Ser	Val	Met
			420					425					430		
His	Glu	Ala	Leu	His	Asn	His	Tyr	Thr	Gln	Lys	Ser	Leu	Ser	Leu	Ser
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Pro	Gly	Lys													
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gcagactccg	tgaagggccg	gttcaccatc	tccagagaca	attccaagaa	cacgctgtat	240
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ggggggggcg	tttgggaccc	cattgactac	tggggccagg	gaaccctggg	caccgtctca	360
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tcaggactct	actccctcag	cagcgtagtg	accgtgccct	ccagcagctt	gggcacccag	600
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<223>  Xaa is varied according to the disclosure

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<400>  29

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Ala Lys His Thr Gly Arg Gly Val Trp Asp Pro Ile Gly Tyr
1           5           10

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<210>  30

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Ala Lys His Thr Gly Gly Gly Val Trp Asp Pro Ile Lys His  
 1 5 10

<210> 31  
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Ala Lys His Thr Gly Gly Gly Val Trp Asp Pro Ile Gly Tyr  
 1 5 10

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Ala Ile His Thr Gly Gly Gly Val Trp Asp Pro Ile Lys Tyr  
 1 5 10

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<223> n is varied according to the disclosure

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<222> (1)..(90)

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<222> (1)..(90)

<223> n=a,c,g, or t

<400> 36

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60

mnnmnnmnnnt ttgcacaat aatatacggc

90

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 <223> n=a,c,g, or t

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 cccggtatgt ttgcacaat aatatacggc 90

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<400> 38  
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<210> 39  
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<400> 39  
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<210> 40  
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 <212> PRT  
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<400> 40

Pro Asp Thr Arg Pro Ala Pro Gly Ser Thr Ala Pro Pro Ala Leu  
 1 5 10 15

<210> 41  
 <211> 16  
 <212> PRT

<213> synthetic

<400> 41

Ala	Lys	His	Asn	Thr	Ser	Lys	Val	Trp	Asp	Pro	Ile	Asp	Tyr	Trp	Gly
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<211> 48

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<213> synthetic

<400> 42

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48

<210> 43

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<212> PRT

<213> synthetic

<400> 43

Ala	Lys	Ser	Ser	Thr	Thr	Thr	Val	Trp	Asp	Pro	Ile	Asp	Tyr	Trp	Gly
1				5				10						15	

<210> 44

<211> 48

<212> DNA

<213> synthetic

<400> 44

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48

<210> 45

<211> 16

<212> PRT

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<220>

<221> PEPTIDE

<222> (1)..(16)

<223> Xaa is varied according to the disclosure

<400> 45

Ala Lys Xaa Pro Met Ala Asn Val Trp Asp Pro Ile Asp Tyr Trp Gly  
 1 5 10 15

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<400> 46  
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48

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 <212> PRT  
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<220>  
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 <222> (1)..(16)  
 <223> Xaa is varied according to the disclosure

<400> 47

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 1 5 10 15

<210> 48  
 <211> 48  
 <212> DNA  
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<400> 48  
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48

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<400> 49

Tyr Trp Gly  
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 <211> 48  
 <212> DNA  
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<400> 50  
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48

<210> 51  
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<400> 51

Ala Lys Arg Tyr Leu Tyr Asp Val Trp Asp Pro Ile Asp Tyr Trp Gly  
 1 5 10 15

<210> 52  
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 <212> DNA  
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<400> 52  
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48

<210> 53  
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<400> 53

Ala Lys His Thr Gly Gly Gly Thr Leu Gln Arg Leu Asp Tyr Trp Gly  
 1 5 10 15

<210> 54  
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<400> 54  
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48

<210> 55  
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<400> 55

Ala	Lys	His	Thr	Gly	Gly	Gly	Thr	Gln	Thr	Pro	Cys	Asp	Tyr	Trp	Gly
1				5				10						15	

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 <212> DNA  
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<400> 56

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48

<210> 57  
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<400> 57

Ala	Lys	His	Thr	Gly	Gly	Gly	Arg	Arg	Ile	Cys	His	Asp	Tyr	Trp	Gly
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48

<210> 59  
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<223> Xaa is varied according to the disclosure

<400> 59

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<212> DNA

<213> synthetic

<400> 60

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48

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<212> PRT

<213> synthetic

<400> 61

Ala	Lys	His	Thr	Gly	Gly	Gly	Gln	Lys	Leu	Gln	Leu	Asp	Tyr	Trp	Gly
1				5				10						15	

<210> 62

<211> 48

<212> DNA

<213> synthetic

<400> 62

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48

<210> 63

<211> 16

<212> PRT

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<220>

<221> PEPTIDE

<222> (1)..(16)

<223> Xaa may be varied according to the disclosure to form alternate peptide



&lt;400&gt; 63

Ala Xaa His Thr Gly Gly Arg Gly Trp Asp Pro Ile Asp Tyr Trp Gly  
 1 5 10 15

&lt;210&gt; 64

&lt;211&gt; 48

&lt;212&gt; DNA

&lt;213&gt; synthetic

&lt;400&gt; 64

gcgtsacata cgggggggcg cggttgggac cccattgact actggggc

48

&lt;210&gt; 65

&lt;211&gt; 16

&lt;212&gt; PRT

&lt;213&gt; synthetic

&lt;400&gt; 65

Ala Asn Gln Thr Gly Gly Gly Val Trp Asp Pro Ile Asp Tyr Trp Gly  
 1 5 10 15

&lt;210&gt; 66

&lt;211&gt; 48

&lt;212&gt; DNA

&lt;213&gt; synthetic

&lt;400&gt; 66

gcgaaccaga ctgggggggg cgtttgggac cccattgact actggggc

48

&lt;210&gt; 67

&lt;211&gt; 16

&lt;212&gt; PRT

&lt;213&gt; synthetic

&lt;400&gt; 67

Ala Arg His Thr Gly Gly Gly Val Trp Asp Pro Ile Tyr Tyr Trp Gly  
 1 5 10 15

&lt;210&gt; 68

&lt;211&gt; 48

&lt;212&gt; DNA

<213> synthetic

<400> 68

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<211> 16

<212> PRT

<213> synthetic

<400> 69

Ala	Lys	Pro	Thr	Gly	Gly	Gly	Ala	Trp	Asp	Pro	Ile	Asp	Tyr	Trp	Gly
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<211> 48

<212> DNA

<213> synthetic

<400> 70

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<211> 16

<212> PRT

<213> synthetic

<400> 71

Ala	Lys	His	Thr	Gly	Val	Gly	Val	Trp	His	Pro	Ile	Tyr	Tyr	Trp	Gly
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<212> DNA

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<400> 72

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48

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<212> PRT

<213> synthetic

<400> 73

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<400> 74

Ala Lys His Thr Gly Glu Gly Val Trp Asp Pro Ile Lys Tyr  
1 5 10

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<400> 75

Ala Lys His Thr Gly Gly Gly Val Trp Asp Pro Ile Asp Lys  
1 5 10

<210> 76

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<400> 76

Ala Lys His Thr Gly Gly Gly Val Trp Asp Pro Ile Gly Tyr  
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<210> 77

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<400> 77

Ala Arg His Thr Gly Gly Gly Val Trp Asp Pro Ile Gly Tyr  
1 5 10

<210> 78  
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<400> 78

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<210> 79  
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Ala Lys His Thr Gly Gly Gly Val Trp Asp Pro Ile Gly His  
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<210> 80  
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<400> 80

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Ala Lys His Thr Gly Gly Gly Val Trp Asp Pro Leu Gly Tyr  
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<210> 82  
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<400> 82

Ala Lys His Thr Gly Gly Gly Val Trp Asp Pro Leu Asp Asn  
1 5 10

<210> 83  
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<400> 83

Ala Lys His Thr Gly Gly Gly Val Trp Asp Pro Ile Asn Tyr  
1 5 10

<210> 84  
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<400> 84

Ala Arg His Thr Gly Gly Gly Val Trp Asp Pro Ile Asn Tyr  
1 5 10

<210> 85  
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<400> 85

Ala Lys His Thr Gly Ser Gly Val Trp Asp Pro Ile Asn Tyr  
1 5 10

<210> 86  
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<400> 86

Ala Lys His Thr Gly Gly Gly Val Trp Asp Pro Ile Asn Asp  
1 5 10

<210> 87  
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<400> 87

Ala Lys His Thr Gly Val Gly Val Trp Asp Pro Met Asn Tyr  
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<210> 88

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<400> 88

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<400> 89

Ala Lys His Thr Gly Gly Gly Val Trp Asp Pro Ile Ala Tyr  
1 5 10

<210> 90

<211> 14

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<400> 90

Ala Lys His Thr Gly Gly Gly Val Trp Asp Pro Ile Ala Asn  
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<210> 91

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<400> 91

Ala Lys His Thr Gly Gly Gly Val Trp Asp Pro Phe Ala Tyr  
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<210> 92

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<400> 92

Ala Lys His Thr Gly Gly Gly Val Trp Asp Pro Met Ala Ser  
1 5 10

<210> 93  
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<400> 93

Ala Lys His Thr Gly Gly Gly Val Trp Asp Pro Met Asp Tyr  
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<210> 94  
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<400> 94

Ala Lys His Thr Gly Gly Gly Val Trp Asp Pro Ile His Tyr  
1 5 10

<210> 95  
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1 5 10

<210> 97  
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Ala Lys His Thr Gly Gly Gly Val Trp Asp Pro Ile Asp Asp  
 1 5 10

<210> 98  
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<400> 98

Val Lys His Thr Gly Gly Gly Val Trp Asp Pro Ile Val Tyr  
 1 5 10

<210> 99  
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<400> 99

Ala Lys His Thr Gly Gly Gly Val Trp Asp Pro Val Asp Tyr  
 1 5 10

<210> 100  
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<400> 100

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 1 5 10

<210> 101  
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<400> 101

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1 5 10

<210> 102

<211> 14

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<400> 102

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<210> 103

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<400> 103

Ala Lys His Thr Gly Gly Gly Val Trp Asp Pro Met His Tyr  
1 5 10

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<211> 14

<212> PRT

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<400> 104

Ala Lys His Thr Gly Gly Gly Val Trp Asn Pro Ile Asp Tyr  
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<210> 105

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<400> 105

Val Lys His Thr Gly Gly Gly Val Trp Asp Pro Ile Asp Tyr  
1 5 10

<210> 106

<211> 14

<212> PRT  
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<400> 106

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<210> 107  
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<400> 107

Ala Gln His Thr Gly Gly Gly Val Trp Asp Pro Ile Gly Tyr  
 1 5 10

<210> 108  
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<400> 108

Ala Lys His Thr Gly Arg Gly Val Trp Asp Pro Ile Asp Tyr  
 1 5 10

<210> 109  
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<400> 109

Ala Lys His Thr Gly Gly Gly Val Trp Asp Pro Ile Tyr Tyr  
 1 5 10

<210> 110  
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 <212> DNA  
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<400> 110

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gtacag 66

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tggtcccagg gcc 73

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